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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=12; day=18; hr=15; min=25; sec=51; ms=357;  
]

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Application No: 10552949 Version No: 1.0

Input Set:

Output Set:

Started: 2008-12-01 18:51:30.378  
Finished: 2008-12-01 18:51:31.157  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 779 ms  
Total Warnings: 9  
Total Errors: 0  
No. of SeqIDs Defined: 9  
Actual SeqID Count: 9

Error code	Error Description
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# SEQUENCE LISTING

<110> Omary, Bishr  
Ku, Nam-Om

<120> Keratin 8 and 18 mutations are Risk  
Factors for Developing Liver Disease of Multiple Etiologies

<130> STAN-297WO

<140> 10552949

<141> 2008-12-01

<150> 60/462,989

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agc ttc acc act	cgc tcc acc ttc	tcc acc aac tac	cgg tcc ctg	ggc		166
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tct gtc cag gcg	ccc agc tac ggc	gcc cgg ccg gtc	agc agc gcg gcc			214
Ser Val Gln Ala	Pro Ser Tyr Gly	Ala Arg Pro Val	Ser Ser Ala Ala			
	20	25	30			
agc gtc tat gca	ggc gct ggg ggc	tct ggt tcc cgg	atc tcc gtg tcc			262
Ser Val Tyr Ala	Gly Ala Gly Gly	Ser Gly Ser Arg	Ile Ser Val Ser			
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cgc tcc acc agc	ttc agg ggc ggc	atg ggg tcc ggg	ggc ctg gcc acc			310
Arg Ser Thr Ser	Phe Arg Gly Gly	Met Gly Ser Gly	Gly Leu Ala Thr			
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ggg ata gcc ggg	ggt ctg gca gga	atg gga ggc atc	cag aac gag aag			358
Gly Ile Ala Gly	Gly Leu Ala Gly	Met Gly Gly Ile	Gln Asn Glu Lys			
65	70	75	80			
gag acc atg caa	agc ctg aac gac	cgc ctg gcc tct	tac ctg gac aga			406
Glu Thr Met Gln	Ser Leu Asn Asp	Arg Leu Ala Ser	Tyr Leu Asp Arg			

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Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg			
100	105	110	
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Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr			
115	120	125	
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Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val			
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Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala			
145	150	155	160
gat gac ttt aga gtc aag tat gag aca gag ctg gcc atg cgc cag tct			646
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165	170	175	
gtg gag aac gac atc cat ggg ctc cgc aag gtc att gat gac acc aat			694
Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr Asn			
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Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln			
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Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys			
225	230	235	240
tct cag gac ctc gcc aag atc atg gca gac atc cgg gcc caa tat gac			886
Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp			
245	250	255	
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Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln			
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Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val			
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Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln	
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Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg	
340 345 350	
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Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile	
355 360 365	
aag gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa	1270
Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu	
370 375 380	
gat gcc gag gac ttt aat ctt ggt gat gcc ttg gac agc agc aac tcc	1318
Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser	
385 390 395 400	
atg caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa	1366
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gtg gtg tct gag acc aat gac acc aaa gtt ctg agg cat taa	1408
Val Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His *	
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Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg	
85 90 95	
Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg	
100 105 110	
Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His Tyr	
115 120 125	
Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr Val	
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Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala Ala	

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Val	Glu	Asn	Asp	Ile	His	Gly	Leu	Arg	Lys	Val	Ile	Asp	Asp	Thr	Asn
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225					230					235				240	
Ser	Gln	Asp	Leu	Ala	Lys	Ile	Met	Ala	Asp	Ile	Arg	Ala	Gln	Tyr	Asp
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			260					265					270		
Gln	Ile	Glu	Glu	Ser	Thr	Thr	Val	Val	Thr	Thr	Gln	Ser	Ala	Glu	Val
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Gly	Ala	Ala	Glu	Thr	Thr	Leu	Thr	Glu	Leu	Arg	Arg	Thr	Val	Gln	Ser
		290				295					300				
Leu	Glu	Ile	Asp	Leu	Asp	Ser	Met	Arg	Asn	Leu	Lys	Ala	Ser	Leu	Glu
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		340					345					350			
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		355				360						365			
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385					390					395				400	
Met	Gln	Thr	Ile	Gln	Lys	Thr	Thr	Thr	Arg	Arg	Ile	Val	Asp	Gly	Lys
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ccc cgg gcc ttc agc agc cgc tcc tac acg agt ggg ccc ggt tcc cgc	155
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atc agc tcc tcg agc ttc tcc cga gtg ggc agc agc aac ttt cgc ggt	203

Ile Ser Ser Ser Ser Phe Ser Arg Val Gly Ser Ser Asn Phe Arg Gly	
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Gly Leu Gly Gly Gly Tyr Gly Gly Ala Ser Gly Met Gly Gly Ile Thr	
50 55 60	
gca gtt acg gtc aac cag agc ctg ctg agc ccc ctt gtc ctg gag gtg	299
Ala Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val	
65 70 75	
gac ccc aac atc cag gcc gtg cgc acc cag gag aag gag cag atc aag	347
Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys	
80 85 90 95	
acc ctc aac aac aag ttt gcc tcc ttc ata gac aag gta cgg ttc ctg	395
Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu	
100 105 110	
gag cag cag aac aag atg ctg gag acc aag tgg agc ctc ctg cag cag	443
Glu Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln	
115 120 125	
cag aag acg gct cga agc aac atg gac aac atg ttc gag agc tac atc	491
Gln Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile	
130 135 140	
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Asn Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys	
145 150 155	
ctg gag gcg gag ctt ggc aac atg cag ggg ctg gtg gag gac ttc aag	587
Leu Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys	
160 165 170 175	
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180 185 190	
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Phe Val Leu Ile Lys Lys Asp Val Asp Glu Ala Tyr Met Asn Lys Val	
195 200 205	
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Glu Leu Glu Ser Arg Leu Glu Gly Leu Thr Asp Glu Ile Asn Phe Leu	
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Arg Gln Leu Tyr Glu Glu Glu Ile Arg Glu Leu Gln Ser Gln Ile Ser	
225 230 235	
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Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp Met	
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275	280	285	
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Ile Glu Gly Leu Lys Gly Gln Arg Ala Ser Leu Glu Ala Ala Ile Ala			
320	325	330	335
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Asp Ala Glu Gln Arg Gly Glu Leu Ala Ile Lys Asp Ala Asn Ala Lys			
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370	375	380	
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420	425	430	
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Pro Gly Leu Ser Tyr Ser Leu Gly Ser Ser Phe Gly Ser Gly Ala Gly			
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Leu Pro Lys *			
480			



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      50             55             60
Val Thr Val Asn Gln Ser Leu Leu Ser Pro Leu Val Leu Glu Val Asp
65             70             75             80
Pro Asn Ile Gln Ala Val Arg Thr Gln Glu Lys Glu Gln Ile Lys Thr
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Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu Glu
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Gln Gln Asn Lys Met Leu Glu Thr Lys Trp Ser Leu Leu Gln Gln Gln
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Lys Thr Ala Arg Ser Asn Met Asp Asn Met Phe Glu Ser Tyr Ile Asn
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Asn Leu Arg Arg Gln Leu Glu Thr Leu Gly Gln Glu Lys Leu Lys Leu
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Glu Ala Glu Leu Gly Asn Met Gln Gly Leu Val Glu Asp Phe Lys Asn
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Lys Tyr Glu Asp

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